

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:	/ o /080,959
Source:	OIPE
Date Processed by STIC:	3/11/2002

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216. PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax) PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

http://www.uspto.gov/web/offices/pac/checker

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

- 1. EFS-Bio (http://www.uspto.gov/ebc/efs/downloads/documents.htm, EFS Submission User Manual ePAVE)
- 2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
- Hand Carry directly to:
 U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202

U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202



OIPE

RAW SEQUENCE LISTING

DATE: 03/11/2002

PATENT APPLICATION: US/10/080,959

TIME: 10:19:07

Input Set : A:\EP.txt

Output Set: N:\CRF3\03112002\J080959.raw

Does Not the party cares' 180 3'5 0

2 <110 > APPLICANT: Cruz-Perez, Patricia

Buttner, Mark P.

siepp 1-2

W--> 4 <120> TITLE OF INVENTION: Method for Detection of Stachybotrys chartarum in Pure Culture and Field

W--> 5 Samples Using Quantitative Polymerase Chain Reaction

W--> 7 <140> FILE REFERENCE: 0001-00001
W-> 7 <140> CURRENT APPLICATION NUMBER:
C-> 8 <141> CURRENT FILING DAMP

8 <141> CURRENT FILING DATE: 2002-02-22

9 <150> PRIOR APPLICATION NUMBER: US 60/280,712

10 <151> PRIOR FILING DATE: 2001-03-29

W--> 11 <160> NUMBER OF SEQ ID: 5

ERRORED SEQUENCES

W--> 12 <210> SEQ ID NO: 1

13 -: 211> LENGTH: 17

14 -: 212 > TYPE: DNA

15 -213> ORGANISM: Stachybotrys chartarum

V++> 16 <220> FEATURE:

-> 17 <221> NAME/KEY: 18 + .222 > LOCATION:

19 <223» OTHER INFORMATION:

20 <400> 1

20 (400) 1

20 gttgetteggegggaac insulid

21 · ETO: SEQ ID NO: 2 (see below)

22 · ETO: LENGTH: 20

(global errors)

E--> 20 <400> 1 E--> 20 gttgcttcggcgggaac invelid

23 - 212 - TYPE: DNA

24 + 213 + OEGANISM: Stachybotrys chartarum

W--> 25 <220> FEATURE:

W--> 26 <221> NAME/KEY:

 $27 + 222 \Rightarrow LOCATION:$

28 (223) OTHER INFORMATION: Admin it was

E--> 29 <400> SEQUENCE: 0

E--> 29 tttgcgtttgccactcagag

30 + 210 > SEQ ID NO: 3

seil non-coding nucleatede 11/6/5 with the good

- * * LLU + FEATURE:

W--> 35 <221> NAME/KEY:

SO LZZ - IOCATION:

37 - 223 - OTHER INFORMATION:

F--> 38 <400> SEQUENCE: 0

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/080,959

DATE: 03/11/2002 TIME: 10:19:07

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Output Set: N:\CRF3\03112002\J080959.raw 20111

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W--> 44 <221> NAME/KEY:

45 <222> LOCATION:

same 46 <223> OTHER INFORMATION:

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E--> 47 gcgtttgccactcagagaatact

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50 <212> TYPE: DNA

51 <213> ORGANISM: Stachybotrys chartarum

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W--> 53 <221> NAME/KEY:

54 <222> LOCATION:

55 <223> OTHER INFORMATION: Jane

E--> 56 <400> SEQUENCE: 0

E--> 56 ctgcgcccggatccaggc

Please sei sample Seguene Listing (axialed) for rabid formet. alie, pluse consult dequire Rule:

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Smith, John: Smithgene Inc.
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 <120>
               Example of a Sequence Listing
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 <130>
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<210>
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                                                                  tgggttccgc
rgalgtggca
                                        cttttcagcc
                                                     aggettaggg
             attgctggca
                          gigccacagg
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ctctcgctct

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*:***** :

trees consult

cgcgctcctc

cgcggcgcgg

cggcccctct

Appendix 3, page 2

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ttg Leu	tet Ser	ttc Phe	aaa Lys 10	tgg Trp	cct Pro		ttt Phc	tgt Cys 15	t t g Leu	ttt Phe	gtt Val	tgt Cys	ttg Leu 20	ttc Phe	caa Cln	344
tgt Cys	ccc Pro	aaa Lys 25	gtc -Val	ctc Leu	ccc	tgt Cys	cac His	tca Ser	tca Ser	ctg -Leu	cag Gln	ccg Pro		Ctt u id e.		389
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[Annex VIII follows]

E

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table. The numeric identifier shall be used only in the equence Listing." The order and presentation of the items of information in the "Sequence Listing" shall conform to the arrangement given below. Each item of information shall begin on a new line and shall begin with the numeric identifier enclosed in angle brackets as shown. The submission of those items of information designated with an "M" is mandatory. The submission of those items of information designated with an "O" is optional. Numeric identifiers <110> through <170> shall only be set forth at the beginning of the "Sequence Listing." The following table illustrates the numeric identifiers.

requirements to Till

Numeric Identifier	Definition	Comments and Format	Mandatory (M) or . Optional (O)
<110>	Applicant	Preferably max. of 10 names; one name per line; preferable format: Surname, Other. Names and/or Initials	M y
<120>	Title of Invention		М
<130>	File Reference	Personal file reference	M_when filed prior to assignment of appl. number
<140>	Current Applica- tion Numbér	Specify as: US 07/999,999 or PCT/US96/99999	M, if available
<141>	Current Filing Date	Specify as: yyyy-mm-dd	f M, if available
<150>	Prior Application Number	Specify as: US 07/999,999 or PCT/US96/99999	M, if applicable include priority documents under 35 USC 119 and 120
<151>	Prior Application Filing Date	Specify as: yyyy-mm-dd	M, if applicable
<160>	Number of SEQ ID NOs	Count includes total number of SEQ ID NOs	М
<170>	Software . T	Name of software used to create the Sequence Listing	O E
<210>	SEQ ID NO: #:	Response shall be an integer representing the SEQ ID NO shown	м

...

antur:

Whether presented sequence moleculc is DNA, RNA, or PRT (protein). If . a nucleotide sequence contains both DNA and RNA fragments, the type shall be "DNA." In addition, the combined DNA/ RNA molecule shall be further described in the <220> to <223> [cature section.

<213>

Organism

Scientific name, i.e. Genus/species, Unknown or Artificial Sequence. In addition, the "Unknown" or "Artificial Scquence" organisms shall be further described in the <220> to <223> feature section.

<220>

Feature

7,4

Leave blank after <220>. <221-223> provide for a description of points of biological significance in the sequence.

M, under the (ollowing conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified base was used in a sequence; if ORGAN-ISM is "Artificial Sequence" or "Unknown"; if molecule is combined DNA/RNA.

<221>

Name/Key

Provide appropriate identifier for feature, pre-(crably from WIPO Standard ST. 25 (1998), Appendix 2, Tables 5 and 6

M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified base was used in a sequence

<2225

Incation

Specify location

M under the fol-

1 1051

d: acid or modified

bases/amino acids

WARRING COPY

Other relevant

c	wa s	uso≱d	in_
сq	uenc	c	_

M, under the fol-

<223>	Other Infor- mation	Other relevant information; four lines maximum	M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified base was used in a sequence; if			
:	*	· × .	ORGANISM is "Artificial Sequence" or			
			"Unknown"; if ===================================			
<300> :	Publication Information	Leave blank ¹ after <300> /-	0			
<301>	Authors	Preferably max of ten named authors of publi- cation; specify one name per line; preferable format: Surname, Other Names and/or Initials	: ¥ 0			
<302>	Title		0			
<303>	; Journal		0			
<304>	Volume		0			
<305>	Issue	÷	0			
<306>	Pages		O ·			
<307>	Date	Journal date on which data published; specify as yyyy-mm-dd, 1994-yyyy or Season-yyyy	0			
< 300>	Dalabase Accession Number	Accession number assigned by data-base including database name	0			
<309>	Database Entry Date	Date of entry in database; specify as yyyy-mm-dd or MM-yyyy	0			
<310>	Patent Document	Document number;	O			

*:

<311>	Patent File) Date	Document filing date, for patent-type citations only; specify as yyyy-mm-d	d .	•
<312>	Publication Date	Document publication date, for patent-type citations only; specify as yyyy-mm-do	, see	
<313>	Relevant Residues	FROM (position) TO (position)	0	•==
<400> .·	Sequence	SEQ ID NO should follow the numeric identifier and should appear on the line preceding the actual sequence		

5. Section 1.024 is revised to read as follows:

- 1.024 Form and format for nucleotide and/or amino acid sequence submissions in computer readable form.
- (a) The computer readable form required by 1.021(c) shall meet the following specifications:

-::::

- (1) The computer readable form shall contain a single "Sequence Listing" as either a diskette, series of diskettes, or other permissible media outlined in paragraph (c) of this section.
- (2) The "Sequence Listing" in paragraph (a) (1) of this section shall be submitted in American Standard Code for Information Interchange (ASCII) text. No other formats shall be allowed.
- (3) The computer readable form may be created by any means, such as word processors, nucleotide/amino acid sequence editors or other custom computer programs; however, it shall conform to all specifications detailed in this section.
- (4) File compression is acceptable when using diskette media, so long as the compressed file is in a self-extracting format that will decompress on one of the systems described in paragraph (b) of this section.
- (5) Page numbering shall not appear within the computer readable form version of the "Sequence Listing" file.
- (6) All computer readable forms shall have a label permanently affixed thereto on which has been hand-printed or typed: the name of the applicant, the title of the invention, the date on which the data were recorded on the computer readable form, the operating system used, a reference number, and an application serial number and filing date, if known.
- (b) Computer readable form submissions must meet these format

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/080,959

DATE: 03/11/2002 TIME: 10:19:08

Input Set : A:\EP.txt

L:56 M:283 W: Missing Blank Line separator, <400> field identifier L:56 M:252 E: No. of Seq. differs, <211>LENGTH:Input:18 Found:0 SEQ:5

Output Set: N:\CRF3\03112002\J080959.raw

L:4 M:283 W: Missing Blank Line separator, <120> field identifier L:6 M:283 W: Missing Blank Line separator, <130> field identifier L:7 M:283 W: Missing Blank Line separator, <140> field identifier L:8 M:271 C: Current Filing Date differs, Replaced Current Filing Date L:11 M:283 W: Missing Blank Line separator, <160> field identifier L:12 M:283 W: Missing Blank Line separator, <210> field identifier L:16 M:283 W: Missing Blank Line separator, <220> field identifier L:17 M:257 W: Feature value mis-spelled or invalid, <221 > Name/Key for SEQ ID#:1 L:20 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:1 differs:0 L:20 M:283 W: Missing Blank Line separator, <400> field identifier L:20 M:252 E: No. of Seq. differs, <211>LENGTH:Input:17 Found:0 SEQ:1 L:25 M:283 W: Missing Blank Line separator, -:220> field identifier L:26 M:257 W: Feature value mis-spelled or invalid, <221 Name/Key for SEQ ID#:2 L:39 M:312 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:2 differs:0 L:29 M:283 W: Missing Blank Line separator, <400> field identifier L:29 M:252 E: No. of Seq. differs, <211>LENGTH:Input:20 Found:0 SEQ:2 L:34 M:283 W: Missing Blank Line separator, <220> field identifier L:35 M:257 W: Feature value mis-spelled or invalid, -221> Name/Key for SEQ ID#:3 L:38 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:3 differs:0 L:38 M:283 W: Missing Blank Line separator, <400> field identifier L:38 M:252 E: No. of Seq. differs, <211>LENGTH:Input:19 Found:0 SEQ:3 L:43 M:283 W: Missing Blank Line separator, <220> field identifier L:44 M:257 W: Feature value mis-spelled or invalid, (221) Name/Key for SEQ ID#:4 L:47 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:4 differs:0 L:47 M:283 W: Missing Blank Line separator, <400> field identifier L:47 M:252 E: No. of Seq. differs, <211>LENGTH:Input:23 Found:0 SEQ:4 L:52 M:283 W: Missing Blank Line separator, $<\!\!(220\!\!>$ field identifier L:53 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5 $L:56\ M:212\ E:$ (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:5 differs:0